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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/636,259A

DATE: 05/01/2002
TIME: 12:21:17

Input Set : A:\Sequences for 13092.txt
Output Set: N:\CRF3\05012002\I636259A.raw

#D
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5/13/02

3 <110> APPLICANT: Small, Kersten M
4 Liggett, Stephen
6 <120> TITLE OF INVENTION: Alpha-2A-adrenergic receptor polymorphisms
8 <130> FILE REFERENCE: 13092
10 <140> CURRENT APPLICATION NUMBER: 09/636,259A
11 <141> CURRENT FILING DATE: 2000-08-10
13 <160> NUMBER OF SEQ ID NOS: 16
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1170
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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27 ttccggcaagg ctgggtgcga gatctacctg ggcgtcgacg tgctttctg cactcgatcc 180
29 atcgatcgacc tggcgccat cagcctggac cgctactgtt ccatcacaca ggccatcgag 240
31 tacaacctga agcgacgccc ggcgcgtatc aaggccatca tcattaccgt gtgggtcatc 300
33 tcggccgtca ttccttccc ggcgtatc tccatcgaga agaaggccgg cggccggcgc 360
35 ccgcaggccgg ccgagcccg ctgcgagatc aacgaccaga atggtagatc catctcgatc 420
37 tgcattcgatc cttcttcgc tccctgcctc atcatgatcc tggctacgt ggcgtatc 480
39 cagatcgcca agcgatcgac ccgcgtgcga cccagccgg ggggtccgg cggccgtcgcc 540
41 ggcgcgcggg ggggcaccga ggcaggccc aacggatcg aacggatcg cagcgcgggc 600
43 ccggggggcg cagaggccga accgatcgcc acccagatca acggccccc tggcgagccc 660
45 ggcgcgcgcg ggcgcgcga caccgacgcg ctggacatgg agagatcg gtcttcggac 720
47 cacgcgcgac ggcctccagg gccccgcaga cccgagccgg gtcccccggg caaaggcaag 780
49 gcccgcgac gccaggatcg gccggccgc acgatcgcc ggcgcggcc gggggcgacg 840
51 gggatcgatc cgccggctgc agggccgggg gaggagccgg tcggggctgc caaggatcg 900
53 cgctggcgcg ggcggcagaa ccgcgagaag cgatcgatc tggatcgatc cgtggatcg 960
55 ggatcgatc tggatcgatc gttcccttc ttcttcacat acatcgatc ggcgtcgcc 1020
57 tgctccgtgc cacgcacgt cttcaattc ttcttcgtt tggatcgatc caacatcg 1080
59 ttgaacccgg tcatctacat catctcaac cacgatcc ggcgcgcctt caagaagatc 1140
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66 <212> TYPE: DNA
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
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72 ggcggccccc gggccacccc ttactccctg caggatcgacgc tgacgatcgatc gtgcctggcc 120
74 ggcctgcata tgctgcata cgtgtcgac aacgtgcgt tcattatcgatc cgtgttcacg 180
76 agccgcgcgc tcaaggcgcc ccaaaacctc ttctgggtgt ctctggcctc ggccgacatc 240
78 ctggggcca cgctcgat cccttctcg ctggccaaacg aggtcatggg ctactggtag 300

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80	ttcggcaagg	cttggtgca	gatctacctg	gcgcgtcgacg	tgctttctg	cacgtcgcc	360										
82	atcgtgcacc	tgtgcgccat	cagcctggac	cgtacttgt	ccatcacaca	ggccatcgag	420										
84	tacaacctga	agcgcacgcc	gcgcgcgc	aaggccatca	tcatcaccgt	gtgggtcatc	480										
86	tcggccgtca	tctccttccc	gccgctcatc	tccatcgaga	agaagggcgg	cggcggcggc	540										
88	ccgcagccgg	ccgagccg	ctgcgagatc	aacgaccaga	agtggta	catctcg	600										
90	tgcacatcggt	ccttcttcgc	tccctgcctc	atcatgatcc	tggta	gcatctac	660										
92	cagatcgcca	agcgtcgac	ccgcgtgcca	cccagccggc	gggtccgga	cgcgtcgcc	720										
94	gcgcgcgcgg	ggggcaccga	gcgcaggccc	aagggtctgg	gccccgagcg	cagcgcggc	780										
96	ccggggggcg	cagaggccga	accgctgccc	accagctca	acggcgc	tggcgagccc	840										
98	gcgcgcgcgg	ggccgcgcga	caccgacgcg	ctggacctgg	aggagagctc	gtttccgac	900										
100	cacgcgcgagc	ggcctccagg	gccccgcaga	cccagcgcg	gtccccgggg	caaaggcaag	960										
102	gcccgcgcga	gccaggtgaa	gccgggcgac	agcctgcgc	ggcgcggg	gggggcgacg	1020										
104	ggatcggg	cgccggctgc	aggggcgggg	gaggagcgcg	tcggggctgc	caaggcgtcg	1080										
106	cgctggcgcg	ggcggcagaa	ccgcgagaag	cgcttacgt	tcgtgctggc	cgtggtc	1140										
108	ggagtgttcg	tggtgtgctg	gttccccttc	ttcttacact	acacgctcac	ggccgtcggg	1200										
110	tgctccgtgc	cacgcacgt	cttcaaattc	ttcttctgg	tcggta	tactg	1260										
112	ttgaacccgg	tcatctacac	catcttcaac	cacgattcc	gccgcgc	caagaagatc	1320										
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125	1			5			10							15			
128	Glu	Ala	Pro	Gly	Gly	Gly	Ala	Arg	Ala	Thr	Pro	Tyr	Ser	Leu	Gln	Val	
129				20			25							30			
132	Thr	Leu	Thr	Leu	Val	Cys	Leu	Ala	Gly	Leu	Leu	Met	Leu	Leu	Thr	Val	
133				35			40							45			
136	Phe	Gly	Asn	Val	Leu	Val	Ile	Ile	Ala	Val	Phe	Thr	Ser	Arg	Ala	Leu	
137				50			55							60			
140	Lys	Ala	Pro	Gln	Asn	Leu	Phe	Leu	Val	Ser	Leu	Ala	Ser	Ala	Asp	Ile	
141				65			70							75			80
144	Leu	Val	Ala	Thr	Leu	Val	Ile	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Val	Met	
145				85			90							95			
148	Gly	Tyr	Trp	Tyr	Phe	Gly	Lys	Ala	Trp	Cys	Glu	Ile	Tyr	Leu	Ala	Leu	
149				100			105							110			
152	Asp	Val	Leu	Phe	Cys	Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	
153				115			120							125			
156	Leu	Asp	Arg	Tyr	Trp	Ser	Ile	Thr	Gln	Ala	Ile	Glu	Tyr	Asn	Leu	Lys	
157				130			135							140			
160	Arg	Thr	Pro	Arg	Arg	Ile	Lys	Ala	Ile	Ile	Ile	Thr	Val	Trp	Val	Ile	
161				145			150							155			160
164	Ser	Ala	Val	Ile	Ser	Phe	Pro	Pro	Leu	Ile	Ser	Ile	Glu	Lys	Lys	Gly	
165				165			170							175			
168	Gly	Gly	Gly	Pro	Gln	Pro	Ala	Glu	Pro	Arg	Cys	Glu	Ile	Asn	Asp		
169				180			185							190			
172	Gln	Lys	Trp	Tyr	Val	Ile	Ser	Ser	Cys	Ile	Gly	Ser	Phe	Phe	Ala	Pro	
173				195			200							205			

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176 Cys Leu Ile Met Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys
177 210 215 220
180 Arg Arg Thr Arg Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Val Ala
181 225 230 235 240
184 Ala Pro Pro Gly Gly Thr Glu Arg Arg Pro Asn Gly Leu Gly Pro Glu
185 245 250 255
188 Arg Ser Ala Gly Pro Gly Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln
189 260 265 270
192 Leu Asn Gly Ala Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Thr
193 275 280 285
196 Asp Ala Leu Asp Leu Glu Glu Ser Ser Ser Ser Asp His Ala Glu Arg
197 290 295 300
200 Pro Pro Gly Pro Arg Arg Pro Glu Arg Gly Pro Arg Gly Lys Gly Lys
201 305 310 315 320
204 Ala Arg Ala Ser Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly
205 325 330 335
208 Pro Gly Ala Thr Gly Ile Gly Thr Pro Ala Ala Gly Pro Gly Glu Glu
209 340 345 350
212 Arg Val Gly Ala Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg
213 355 360 365
216 Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val
217 370 375 380
220 Val Cys Trp Phe Pro Phe Phe Thr Tyr Thr Leu Thr Ala Val Gly
221 385 390 395 400
224 Cys Ser Val Pro Arg Thr Leu Phe Lys Phe Phe Trp Phe Gly Tyr
225 405 410 415
228 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp
229 420 425 430
232 Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg
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236 Ile Val
237 450
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241 <211> LENGTH: 450
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 4
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248 1 5 10 15
251 Glu Ala Pro Gly Gly Ala Arg Ala Thr Pro Tyr Ser Leu Gln Val
252 20 25 30
255 Thr Leu Thr Leu Val Cys Leu Ala Gly Leu Leu Met Leu Leu Thr Val
256 35 40 45
259 Phe Gly Asn Val Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu
260 50 55 60
263 Lys Ala Pro Gln Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile
264 65 70 75 80
267 Leu Val Ala Thr Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met
268 85 90 95

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271 Gly Tyr Trp Tyr Phe Gly Lys Ala Trp Cys Glu Ile Tyr Leu Ala Leu
 272 100 105 110
 275 Asp Val Leu Phe Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser
 276 115 120 125
 279 Leu Asp Arg Tyr Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys
 280 130 135 140
 283 Arg Thr Pro Arg Arg Ile Lys Ala Ile Ile Thr Val Trp Val Ile
 284 145 150 155 160
 287 Ser Ala Val Ile Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly
 288 165 170 175
 291 Gly Gly Gly Pro Gln Pro Ala Glu Pro Arg Cys Glu Ile Asn Asp
 292 180 185 190
 295 Gln Lys Trp Tyr Val Ile Ser Ser Cys Ile Gly Ser Phe Phe Ala Pro
 296 195 200 205
 299 Cys Leu Ile Met Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys
 300 210 215 220
 303 Arg Arg Thr Arg Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Val Ala
 304 225 230 235 240
 307 Ala Pro Pro Gly Gly Thr Glu Arg Arg Pro Lys Gly Leu Gly Pro Glu
 308 245 250 255
 311 Arg Ser Ala Gly Pro Gly Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln
 312 260 265 270
 315 Leu Asn Gly Ala Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Thr
 316 275 280 285
 319 Asp Ala Leu Asp Leu Glu Glu Ser Ser Ser Ser Asp His Ala Glu Arg
 320 290 295 300
 323 Pro Pro Gly Pro Arg Arg Pro Glu Arg Gly Pro Arg Gly Lys Gly Lys
 324 305 310 315 320
 327 Ala Arg Ala Ser Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly
 328 325 330 335
 331 Pro Gly Ala Thr Gly Ile Gly Thr Pro Ala Ala Gly Pro Gly Glu Glu
 332 340 345 350
 335 Arg Val Gly Ala Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg
 336 355 360 365
 339 Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val
 340 370 375 380
 343 Val Cys Trp Phe Pro Phe Phe Thr Tyr Thr Leu Thr Ala Val Gly
 344 385 390 395 400
 347 Cys Ser Val Pro Arg Thr Leu Phe Lys Phe Phe Phe Trp Phe Gly Tyr
 348 405 410 415
 351 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp
 352 420 425 430
 355 Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg
 356 435 440 445
 359 Ile Val
 360 450
 363 <210> SEQ ID NO: 5
 364 <211> LENGTH: 22
 365 <212> TYPE: DNA

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368 <400> SEQUENCE: 5
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372 <210> SEQ ID NO: 6
373 <211> LENGTH: 23
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375 <213> ORGANISM: Homo sapiens
377 <400> SEQUENCE: 6
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383 <212> TYPE: DNA
384 <213> ORGANISM: Homo sapiens
386 <400> SEQUENCE: 7
387 tcgtcatcat cgccgtgtc 20
390 <210> SEQ ID NO: 8
391 <211> LENGTH: 23
392 <212> TYPE: DNA
393 <213> ORGANISM: Homo sapiens
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400 <211> LENGTH: 24
401 <212> TYPE: DNA
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405 gccatcatca tcaccgtgtg ggtc 24
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409 <211> LENGTH: 23
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435 <210> SEQ ID NO: 13
436 <211> LENGTH: 23
437 <212> TYPE: DNA
438 <213> ORGANISM: Homo sapiens

VERIFICATION SUMMARY

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